

# SEQUENCE LISTING

<110> Mark, Robert

<120> PABLO, A POLYPEPTIDE THAT INTERACTS WITH BCL-XL, AND  
USES RELATED THERETO

<130> GIN-077

<140>

<141>

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 2625

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (243)..(1919)

<400> 1

cttctcttgc acttgcggat gatgaactgg aataacgatg aaagaaagca catccgatct 60

caacattcac gtcttgcctt ataaccgatt aattaattga tccccagcta gactagtgtt 120

ggagaaatca gcatgttaaa acaactgttg atgatagctg ttggagtaaa gttgcagtgg 180

aagctatggc tgcaaaatcg ttaaaatctt caaggtgaac tggcacaaaag gttaaatctca 240

ag atg ccg cta gtg aaa aga aac atc gat cct agg cac ttg tgc cac 287

Met Pro Leu Val Lys Arg Asn Ile Asp Pro Arg His Leu Cys His  
1 5 10 15

aca gca ctg cct aga ggc att aag aat gaa ctg gaa tgt gta acc aat 335

Thr Ala Leu Pro Arg Gly Ile Lys Asn Glu Leu Glu Cys Val Thr Asn  
20 25 30

att tcc ttg gca aat ata att aga caa cta agt agc cta agt aaa tat 383

Ile Ser Leu Ala Asn Ile Ile Arg Gln Leu Ser Ser Leu Ser Lys Tyr  
35 40 45

gct gaa gat ata ttt gga gaa tta ttc aat gaa gca cat agt ttt tcc 431

Ala Glu Asp Ile Phe Gly Glu Leu Phe Asn Glu Ala His Ser Phe Ser  
50 55 60

ttc aga gtc aac tca ttg caa gaa cgt gtg gac agt tta tct gtt agt 479

Phe Arg Val Asn Ser Leu Gln Glu Arg Val Asp Arg Leu Ser Val Ser  
65 70 75

gtt aca cag ctt gat cca aag gaa gaa gaa ttg tct ttg caa gat ata 527

Val Thr Gln Leu Asp Pro Lys Glu Glu Glu Leu Ser Leu Gln Asp Ile  
80 85 90 95

Sequence Listing

aca	atg	agg	aaa	gct	ttc	cga	agt	tct	aca	att	caa	gac	cag	cag	ctt	575
Thr	Met	Arg	Lys	Ala	Phe	Arg	Ser	Ser	Thr	Ile	Gln	Asp	Gln	Gln	Leu	
				100					105				110			
ttc	gat	cgc	aag	act	ttg	cct	att	cca	tta	cag	gag	acg	tac	gat	gtt	623
Phe	Asp	Arg	Lys	Thr	Leu	Pro	Ile	Pro	Leu	Gln	Glu	Thr	Tyr	Asp	Val	
				115					120				125			
tgt	gaa	cag	cct	cca	cct	ctc	aat	ata	ctc	act	cct	tat	aga	gat	gat	671
Cys	Glu	Gln	Pro	Pro	Pro	Leu	Asn	Ile	Leu	Thr	Pro	Tyr	Arg	Asp	Asp	
				130					135				140			
ggt	aaa	gaa	ggt	ctg	aag	ttt	tat	acc	aat	cct	tcg	tat	ttc	ttt	gat	719
Gly	Lys	Glu	Gly	Leu	Lys	Phe	Tyr	Thr	Asn	Pro	Ser	Tyr	Phe	Phe	Asp	
				145					150				155			
cta	tgg	aaa	gaa	aaa	atg	ttg	caa	gat	aca	gag	gat	aag	agg	aag	gaa	767
Leu	Trp	Lys	Glu	Lys	Met	Leu	Gln	Asp	Thr	Glu	Asp	Lys	Arg	Lys	Glu	
				160					165				170			
aag	agg	aag	cag	aag	cag	aaa	aat	cta	gat	cgt	cct	cat	gaa	cca	gaa	815
Lys	Arg	Lys	Gln	Lys	Gln	Lys	Asn	Leu	Asp	Arg	Pro	His	Glu	Pro	Glu	
				180					185				190			
aaa	gtg	cca	aga	gca	cct	cat	gac	agg	cgg	cga	gaa	tgg	cag	aag	ctg	863
Lys	Val	Pro	Arg	Ala	Pro	His	Asp	Arg	Arg	Arg	Glu	Trp	Gln	Lys	Leu	
				195					200				205			
gcc	caa	ggt	cca	gag	ctg	gct	gaa	gat	gat	gct	aat	ctc	tta	cat	aag	911
Ala	Gln	Gly	Pro	Glu	Leu	Ala	Glu	Asp	Asp	Ala	Asn	Leu	Leu	His	Lys	
				210					215				220			
cat	att	gaa	gtt	gct	aat	ggc	cca	gcc	tct	cat	ttt	gaa	aca	aga	cct	959
His	Ile	Glu	Val	Ala	Asn	Gly	Pro	Ala	Ser	His	Phe	Glu	Thr	Arg	Pro	
				225					230				235			
cag	aca	tac	gtg	gat	cat	atg	gat	gga	tct	tac	tca	ctt	tct	gcc	ttg	1007
Gln	Thr	Tyr	Val	Asp	His	Met	Asp	Gly	Ser	Tyr	Ser	Leu	Ser	Ala	Leu	
				240					245				250			
cca	ttt	agt	cag	atg	agt	gag	ctt	ctg	act	aga	gct	gag	gaa	agg	gta	1055
Pro	Phe	Ser	Gln	Met	Ser	Glu	Leu	Leu	Thr	Arg	Ala	Glu	Glu	Arg	Val	
				260					265				270			
tta	gtc	aga	cca	cat	gaa	cca	cct	cca	cct	cca	cca	atg	cat	gga	gca	1103
Leu	Val	Arg	Pro	His	Glu	Pro	Pro	Pro	Pro	Pro	Pro	Met	His	Gly	Ala	
				275					280				285			
gga	gat	gca	aaa	ccg	ata	ccc	acc	tgt	atc	agt	tct	gct	aca	ggt	ttg	1151
Gly	Asp	Ala	Lys	Pro	Ile	Pro	Thr	Cys	Ile	Ser	Ser	Ala	Thr	Gly	Leu	
				290					295				300			
ata	gaa	aat	cgc	cct	cag	tca	cca	gct	aca	ggc	aga	aca	cct	gtg	ttt	1199
Ile	Glu	Asn	Arg	Pro	Gln	Ser	Pro	Ala	Thr	Gly	Arg	Thr	Pro	Val	Phe	
				305					310				315			

gtg agc ccc act ccc cca cct cct cca cca cct ctt cca tct gcc ttg	1247
Val Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro Leu Pro Ser Ala Leu	
320 325 330 335	
tca act tcc tca tta aga gct tca atg act tca act cct ccc cct cca	1295
Ser Thr Ser Ser Leu Arg Ala Ser Met Thr Ser Thr Pro Pro Pro Pro	
340 345 350	
gta cct ccc cca cct cca cct cca gcc act gct ttg caa gct cca gca	1343
Val Pro Pro Pro Pro Pro Pro Pro Ala Thr Ala Leu Gln Ala Pro Ala	
355 360 365	
gta cca cca cct cca gct cct ctt cag att gcc cct gga gtt ctt cac	1391
Val Pro Pro Pro Pro Ala Pro Leu Gln Ile Ala Pro Gly Val Leu His	
370 375 380	
cca gct cct cct cca att gca cct cct cta gta cag ccc tct cca cca	1439
Pro Ala Pro Pro Pro Ile Ala Pro Pro Leu Val Gln Pro Ser Pro Pro	
385 390 395	
gta gct aga gct gcc cca gta tgt gag act gta cca gtt cat cca ctc	1487
Val Ala Arg Ala Ala Pro Val Cys Glu Thr Val Pro Val His Pro Leu	
400 405 410 415	
cca caa ggt gaa gtt cag ggg ctg cct cca ccc cca cca ccg cct cct	1535
Pro Gln Gly Glu Val Gln Gly Leu Pro Pro Pro Pro Pro Pro Pro Pro	
420 425 430	
ctg cct cca cct ggc att cga cca tca tca cct gtc aca gtt aca gct	1583
Leu Pro Pro Pro Gly Ile Arg Pro Ser Ser Pro Val Thr Val Thr Ala	
435 440 445	
ctt gct cat cct ccc tct ggg cta cat cca act cca tct act gcc cca	1631
Leu Ala His Pro Pro Ser Gly Leu His Pro Thr Pro Ser Thr Ala Pro	
450 455 460	
ggt ccc cat gtt cca tta atg cct cca tct cct cca tca caa gtt ata	1679
Gly Pro His Val Pro Leu Met Pro Pro Ser Pro Pro Ser Gln Val Ile	
465 470 475	
cct gct tct gag cca aag cgc cat cca tca acc cta cct gta atc agt	1727
Pro Ala Ser Glu Pro Lys Arg His Pro Ser Thr Leu Pro Val Ile Ser	
480 485 490 495	
gat gcc agg agt gtg cta ctg gaa gca ata cga aaa ggt att cag cta	1775
Asp Ala Arg Ser Val Leu Leu Glu Ala Ile Arg Lys Gly Ile Gln Leu	
500 505 510	
cgc aaa gta gaa gag cag cgt gaa cag gaa gct aag cat gaa cgc att	1823
Arg Lys Val Glu Glu Gln Arg Glu Gln Glu Ala Lys His Glu Arg Ile	
515 520 525	
gaa aac gat gtt gcc acc atc ctg tct cgc cgt att gct gtt gaa tat	1871
Glu Asn Asp Val Ala Thr Ile Leu Ser Arg Arg Ile Ala Val Glu Tyr	
530 535 540	
agt gat tcg gaa gat gat tca gaa ttt gat gaa gta gat tgg ttg gag	1919

SECRET - TOP SECRET

Ser Asp Ser Glu Asp Asp Ser Glu Phe Asp Glu Val Asp Trp Leu Glu  
 545 550 555

taagaaaaat gcattgataa atattacaaa actgaatgca aatgtccttt gtggtgcttg 1979  
 ttcccttgaaa atgtttggtc attctagtgt tttgctttct tttccttata ataaatgacc 2039  
 cttttcctcc ataacttttg atttctaagg aaaatattag catacatttc aaactaaatg 2099  
 ttttacagtg gcttatcttt tttttccccc tgaaaagact aatttgggtca aataaaccac 2159  
 taagtattaa gcatggacag ctgttggttag agtagcagat tcagtttttt gatatatctt 2219  
 aattgtgtac tttgtgaatt ttaatttaaa gaaagcaact gaaattgaaa tcttgagggc 2279  
 agctgtatct actaatgagc cttattccat ttctgtatgt tttaaaagaa gaaacactgc 2339  
 cttgattata cgaatacact cagaaagtac atttagcttg tagtggtgaa ttctcttaaa 2399  
 ggaatgcttg aattttttca ttattgtttt attgttttta tatacttgcc ttatttgaat 2459  
 gtttagcagt atccccctcc cacttatata ttgtgtgata tgattttgct tgcctatagg 2519  
 agttaaaaac ttttccatgt gaaatactct gacttaaaca tacatgtaac ttacataact 2579  
 gttaagaata acagtctgat ttaataaatg gttcatttta aaagtt 2625

<210> 2  
 <211> 559  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Pro Leu Val Lys Arg Asn Ile Asp Pro Arg His Leu Cys His Thr  
 1 5 10 15  
 Ala Leu Pro Arg Gly Ile Lys Asn Glu Leu Glu Cys Val Thr Asn Ile  
 20 25 30  
 Ser Leu Ala Asn Ile Ile Arg Gln Leu Ser Ser Leu Ser Lys Tyr Ala  
 35 40 45  
 Glu Asp Ile Phe Gly Glu Leu Phe Asn Glu Ala His Ser Phe Ser Phe  
 50 55 60  
 Arg Val Asn Ser Leu Gln Glu Arg Val Asp Arg Leu Ser Val Ser Val  
 65 70 75 80  
 Thr Gln Leu Asp Pro Lys Glu Glu Glu Leu Ser Leu Gln Asp Ile Thr  
 85 90 95  
 Met Arg Lys Ala Phe Arg Ser Ser Thr Ile Gln Asp Gln Gln Leu Phe  
 100 105 110  
 Asp Arg Lys Thr Leu Pro Ile Pro Leu Gln Glu Thr Tyr Asp Val Cys  
 115 120 125

bioRxiv preprint doi: <https://doi.org/10.1101/044280>; this version posted February 1, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Glu 130	Gln	Pro	Pro	Pro	Leu	Asn 135	Ile	Leu	Thr	Pro	Tyr 140	Arg	Asp	Asp	Gly
Lys 145	Glu	Gly	Leu	Lys	Phe 150	Tyr	Thr	Asn	Pro	Ser 155	Tyr	Phe	Phe	Asp	Leu 160
Trp	Lys	Glu	Lys	Met 165	Leu	Gln	Asp	Thr	Glu 170	Asp	Lys	Arg	Lys	Glu 175	Lys
Arg	Lys	Gln	Lys 180	Gln	Lys	Asn	Leu	Asp 185	Arg	Pro	His	Glu	Pro 190	Glu	Lys
Val	Pro	Arg 195	Ala	Pro	His	Asp	Arg 200	Arg	Arg	Glu	Trp	Gln 205	Lys	Leu	Ala
Gln	Gly 210	Pro	Glu	Leu	Ala	Glu 215	Asp	Asp	Ala	Asn	Leu 220	Leu	His	Lys	His
Ile 225	Glu	Val	Ala	Asn	Gly 230	Pro	Ala	Ser	His	Phe 235	Glu	Thr	Arg	Pro	Gln 240
Thr	Tyr	Val	Asp	His 245	Met	Asp	Gly	Ser	Tyr 250	Ser	Leu	Ser	Ala	Leu 255	Pro
Phe	Ser	Gln	Met 260	Ser	Glu	Leu	Leu	Thr 265	Arg	Ala	Glu	Glu	Arg 270	Val	Leu
Val	Arg 275	Pro	His	Glu	Pro	Pro 280	Pro	Pro	Pro	Pro	Met	His 285	Gly	Ala	Gly
Asp	Ala 290	Lys	Pro	Ile	Pro	Thr 295	Cys	Ile	Ser	Ser	Ala 300	Thr	Gly	Leu	Ile
Glu 305	Asn	Arg	Pro	Gln	Ser 310	Pro	Ala	Thr	Gly	Arg 315	Thr	Pro	Val	Phe	Val 320
Ser	Pro	Thr	Pro	Pro 325	Pro	Pro	Pro	Pro	Pro 330	Leu	Pro	Ser	Ala	Leu 335	Ser
Thr	Ser	Ser	Leu 340	Arg	Ala	Ser	Met	Thr 345	Ser	Thr	Pro	Pro	Pro 350	Pro	Val
Pro	Pro 355	Pro	Pro	Pro	Pro	Pro	Ala 360	Thr	Ala	Leu	Gln 365	Ala	Pro	Ala	Val
Pro	Pro 370	Pro	Pro	Ala	Pro	Leu 375	Gln	Ile	Ala	Pro	Gly 380	Val	Leu	His	Pro
Ala 385	Pro	Pro	Pro	Ile	Ala 390	Pro	Pro	Leu	Val	Gln 395	Pro	Ser	Pro	Pro	Val 400
Ala	Arg	Ala	Ala	Pro 405	Val	Cys	Glu	Thr	Val 410	Pro	Val	His	Pro	Leu 415	Pro
Gln	Gly	Glu	Val 420	Gln	Gly	Leu	Pro	Pro 425	Pro	Pro	Pro	Pro	Pro 430	Pro	Leu

Pro Pro Pro Gly Ile Arg Pro Ser Ser Pro Val Thr Val Thr Ala Leu  
435 440 445

Ala His Pro Pro Ser Gly Leu His Pro Thr Pro Ser Thr Ala Pro Gly  
450 455 460

Pro His Val Pro Leu Met Pro Pro Ser Pro Pro Ser Gln Val Ile Pro  
465 470 475 480

Ala Ser Glu Pro Lys Arg His Pro Ser Thr Leu Pro Val Ile Ser Asp  
485 490 495

Ala Arg Ser Val Leu Leu Glu Ala Ile Arg Lys Gly Ile Gln Leu Arg  
500 505 510

Lys Val Glu Glu Gln Arg Glu Gln Glu Ala Lys His Glu Arg Ile Glu  
515 520 525

Asn Asp Val Ala Thr Ile Leu Ser Arg Arg Ile Ala Val Glu Tyr Ser  
530 535 540

Asp Ser Glu Asp Asp Ser Glu Phe Asp Glu Val Asp Trp Leu Glu  
545 550 555

<210> 3

<211> 747

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (21)..(656)

<400> 3

cagctttgac tcatatgaaa atg tct cag agc aac cgg gag ctg gtg gtt gac 53  
Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp  
1 5 10

ttt ctc tcc tac aag ctt tcc cag aaa gga tac agc tgg agt cag ttt 101  
Phe Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe  
15 20 25

agt gat gtg gaa gag aac agg act gag gcc cca gaa ggg act gaa tcg 149  
Ser Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser  
30 35 40

gag atg gag acc ccc agt gcc atc aat ggc aac cca tcc tgg cac ctg 197  
Glu Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu  
45 50 55

gca gac agc ccc gcg gtg aat gga gcc act ggc cac agc agc agt ttg 245  
Ala Asp Ser Pro Ala Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu  
60 65 70 75

gat gcc cgg gag gtg atc ccc atg gca gca gta aag caa gcg ctg agg 293

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Asp Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg  
                     80                    85                    90  
 gag gca ggc gac gag ttt gaa ctg cgg tac cgg cgg gca ttc agt gac 341  
 Glu Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp  
                     95                    100                    105  
 ctg aca tcc cag ctc cac atc acc cca ggg aca gca tat cag agc ttt 389  
 Leu Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe  
                     110                    115                    120  
 gaa cag gta gtg aat gaa ctc ttc cgg gat ggg gta aac tgg ggt cgc 437  
 Glu Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg  
                     125                    130                    135  
 att gtg gcc ttt ttc tcc ttc ggc ggg gca ctg tgc gtg gaa agc gta 485  
 Ile Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val  
                     140                    145                    150                    155  
 gac aag gag atg cag gta ttg gtg agt cgg atc gca gct tgg atg gcc 533  
 Asp Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala  
                     160                    165                    170  
 act tac cgg aat gac cac cta gag cct tgg atc cag gag aac ggc ggc 581  
 Thr Tyr Arg Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly  
                     175                    180                    185  
 tgg gat act ttt gtg gaa ctc tat ggg aac aat gca gca gcc gag agc 629  
 Trp Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser  
                     190                    195                    200  
 cga aag ggc cag gaa cgc ttc aac cgc tgagtcgacc tgcagccaag 676  
 Arg Lys Gly Gln Glu Arg Phe Asn Arg  
                     205                    210  
 ctaattccgg gcgaatttct tatgatttat gatttttatt attaaataag ttataaaaaa 736  
 aataagtgtg t 747  
  
 <210> 4  
 <211> 212  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 4  
 Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr Lys  
     1                    5                    10                    15  
 Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val Glu Glu  
                     20                    25                    30  
 Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met Glu Thr Pro  
                     35                    40                    45  
 Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala  
                     50                    55                    60

662607 = T03224.10

```

<210> 5
<211> 1254
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1254)

<400> 5
atg ccg cta gtg aaa aga aac atc gat cct agg cac ttg tgc cac aca 48
Met Pro Leu Val Lys Arg Asn Ile Asp Pro Arg His Leu Cys His Thr
1 5 10 15

gca ctg cct aga ggc att aag aat gaa ctg gaa tgt gta acc aat att 96
Ala Leu Pro Arg Gly Ile Lys Asn Glu Leu Glu Cys Val Thr Asn Ile
20 25 30

tcc ttg gca aat ata att aga caa cta agt agc cta agt aaa tat gct 144
Ser Leu Ala Asn Ile Ile Arg Gln Leu Ser Ser Leu Ser Lys Tyr Ala
35 40 45

gaa gat ata ttt gga gaa tta ttc aat gaa gca cat agt ttt tcc ttc 192
Glu Asp Ile Phe Gly Glu Leu Phe Asn Glu Ala His Ser Phe Ser Phe
50 55 60

```



aga Arg 65	gtc Val	aac Asn	tca Ser	ttg Leu	caa Gln 70	gaa Glu	cgt Arg	gtg Val	gac Asp	cgt Arg 75	tta Leu	tct Ser	gtt Val	agt Ser	gtt Val 80	240
aca Thr	cag Gln	ctt Leu	gat Asp	cca Pro 85	aag Lys	gaa Glu	gaa Glu	gaa Glu	ttg Leu 90	tct Ser	ttg Leu	caa Gln	gat Asp	ata Ile 95	aca Thr	288
atg Met	agg Arg	aaa Lys	gct Ala 100	ttc Phe	cga Arg	agt Ser	tct Ser	aca Thr 105	att Ile	caa Gln	gac Asp	cag Gln 110	cag Gln	ctt Leu	ttc Phe	336
gat Asp	cgc Arg	aag Lys 115	act Thr	ttg Leu	cct Pro	att Ile	cca Pro 120	tta Leu	cag Gln	gag Glu	acg Thr 125	tac Tyr	gat Asp	gtt Val	tgt Cys	384
gaa Glu 130	cag Gln	cct Pro	cca Pro	cct Pro	ctc Leu 135	aat Asn	ata Ile	ctc Leu	act Thr	cct Pro 140	tat Tyr	aga Arg	gat Asp	gat Asp	ggc Gly	432
aaa Lys 145	gaa Glu	ggc Gly	ctg Leu	aag Lys	ttt Phe 150	tat Tyr	acc Thr	aat Asn	cct Pro 155	tcg Ser	tat Tyr	ttc Phe	ttt Phe	gat Asp	cta Leu 160	480
tgg Trp	aaa Lys	gaa Glu	aaa Lys	atg Met 165	ttg Leu	caa Gln	gat Asp	aca Thr 170	gag Glu	gat Asp	aag Lys	agg Arg	aag Lys	gaa Glu 175	aag Lys	528
agg Arg	aag Lys	cag Gln	aag Lys 180	cag Gln	aaa Lys	aat Asn	cta Leu 185	gat Asp	cgt Arg	cct Pro	cat His	gaa Glu 190	cca Pro	gaa Glu	aaa Lys	576
gtg Val	cca Pro 195	aga Arg	gca Ala	cct Pro	cat His	gac Asp	agg Arg 200	cgg Arg	cga Arg	gaa Glu	tgg Trp 205	cag Gln	aag Lys	ctg Leu	gcc Ala	624
caa Gln 210	ggc Gly	cca Pro	gag Glu	ctg Leu	gct Ala 215	gaa Glu	gat Asp	gat Asp	gct Ala	aat Asn 220	ctc Leu	tta Leu	cat His	aag Lys	cat His	672
att Ile 225	gaa Glu	gtt Val	gct Ala	aat Asn	ggc Gly 230	cca Pro	gcc Ala	tct Ser	cat His	ttt Phe 235	gaa Glu	aca Thr	aga Arg	cct Pro	cag Gln 240	720
aca Thr	tac Tyr	gtg Val	gat Asp	cat His 245	atg Met	gat Asp	gga Gly	tct Ser	tac Tyr 250	tca Ser	ctt Leu	tct Ser	gcc Ala 255	ttg Leu	cca Pro	768
ttt Phe	agt Ser	cag Gln	atg Met 260	agt Ser	gag Glu	ctt Leu	ctg Leu	act Thr 265	aga Arg	gct Ala	gag Glu	gaa Glu	agg Arg 270	gta Val	tta Leu	816
gtc Val	aga Arg 275	cca Pro	cat His	gaa Glu	cca Pro	cct Pro	cca Pro 280	cct Pro	cca Pro	cca Pro	atg Met 285	cat His	gga Gly	gca Ala	gga Gly	864



Thr	Gln	Leu	Asp	Pro	Lys	Glu	Glu	Glu	Leu	Ser	Leu	Gln	Asp	Ile	Thr	
				85					90					95		
Met	Arg	Lys	Ala	Phe	Arg	Ser	Ser	Thr	Ile	Gln	Asp	Gln	Gln	Leu	Phe	
				100					105					110		
Asp	Arg	Lys	Thr	Leu	Pro	Ile	Pro	Leu	Gln	Glu	Thr	Tyr	Asp	Val	Cys	
				115					120					125		
Glu	Gln	Pro	Pro	Pro	Leu	Asn	Ile	Leu	Thr	Pro	Tyr	Arg	Asp	Asp	Gly	
				130					135					140		
Lys	Glu	Gly	Leu	Lys	Phe	Tyr	Thr	Asn	Pro	Ser	Tyr	Phe	Phe	Asp	Leu	
				145					150					155		
Trp	Lys	Glu	Lys	Met	Leu	Gln	Asp	Thr	Glu	Asp	Lys	Arg	Lys	Glu	Lys	
				165					170					175		
Arg	Lys	Gln	Lys	Gln	Lys	Asn	Leu	Asp	Arg	Pro	His	Glu	Pro	Glu	Lys	
				180					185					190		
Val	Pro	Arg	Ala	Pro	His	Asp	Arg	Arg	Arg	Glu	Trp	Gln	Lys	Leu	Ala	
				195					200					205		
Gln	Gly	Pro	Glu	Leu	Ala	Glu	Asp	Asp	Ala	Asn	Leu	Leu	His	Lys	His	
				210					215					220		
Ile	Glu	Val	Ala	Asn	Gly	Pro	Ala	Ser	His	Phe	Glu	Thr	Arg	Pro	Gln	
				225					230					235		
Thr	Tyr	Val	Asp	His	Met	Asp	Gly	Ser	Tyr	Ser	Leu	Ser	Ala	Leu	Pro	
				245					250					255		
Phe	Ser	Gln	Met	Ser	Glu	Leu	Leu	Thr	Arg	Ala	Glu	Glu	Arg	Val	Leu	
				260					265					270		
Val	Arg	Pro	His	Glu	Pro	Pro	Pro	Pro	Pro	Pro	Met	His	Gly	Ala	Gly	
				275					280					285		
Asp	Ala	Lys	Pro	Ile	Pro	Thr	Cys	Ile	Ser	Ser	Ala	Thr	Gly	Leu	Ile	
				290					295					300		
Glu	Asn	Arg	Pro	Gln	Ser	Pro	Ala	Thr	Gly	Arg	Thr	Pro	Val	Phe	Val	
				305					310					315		
Ser	Pro	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Ser	Ala	Leu	Ser	
				325					330					335		
Thr	Ser	Ser	Leu	Arg	Ala	Ser	Met	Thr	Ser	Thr	Pro	Pro	Pro	Pro	Val	
				340					345					350		
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Thr	Ala	Leu	Gln	Ala	Pro	Ala	Val	
				355					360					365		
Pro	Pro	Pro	Pro	Ala	Pro	Leu	Gln	Ile	Ala	Pro	Gly	Val	Leu	His	Pro	
				370					375					380		

Ala	Pro	Pro	Pro	Ile	Ala	Pro	Pro	Leu	Val	Gln	Pro	Ser	Pro	Pro	Val
385					390					395					400

Ala Arg Ala Ala Pro Val Cys Glu Thr Val Pro Val His Pro Leu Pro  
405 410 415

Gln Gly

Sur  
at  
cert

[illegible]